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(1) GENERAL INFORMATION:

- (i) APPLICANT: Bakker, Alexander B.H.
Phillips, Joseph H.
Lanier, Lewis L.
- (ii) TITLE OF INVENTION: Mammalian Cell Membrane Proteins;
Related Reagents
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: DNAX Research Institute
 - (B) STREET: 901 California Avenue
 - (C) CITY: Palo Alto
 - (D) STATE: California
 - (E) COUNTRY: USA
 - (F) ZIP: 94304-1104
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US
 - (B) FILING DATE: 31-JUL-1998
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/089,168
 - (B) FILING DATE: 12-JUN-1998
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/069,692
 - (B) FILING DATE: 16-DEC-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/069,639
 - (B) FILING DATE: 15-DEC-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/063,717
 - (B) FILING DATE: 29-OCT-1997
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/054,430
 - (B) FILING DATE: 01-AUG-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Ching, Edwin P.
 - (B) REGISTRATION NUMBER: 34,090
 - (C) REFERENCE/DOCKET NUMBER: DX0763X
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (650)852-9196
 - (B) TELEFAX: (650)496-1200

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 342 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..339

(ix) FEATURE:

- (A) NAME/KEY: mat_peptide
- (B) LOCATION: 79..339

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATG GGG GGA CTT GAA CCC TGC AGC AGG CTC CTG CTC CTG CCT CTC CTG	48
Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu	
-26 -25 -20 -15	
CTG GCT GTA AGT GGT CTC CGT CCT GTC CAG GCC CAG GCC CAG AGC GAT	96
Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln Ala Gln Ser Asp	
-10 -5 1 5	
TGC AGT TGC TCT ACG GTG AGC CCG GGC GTG CTG GCA GGG ATC GTG ATG	144
Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met	
10 15 20	
GGA GAC CTG GTG CTG ACA GTG CTC ATT GCC CTG GCC GTG TAC TTC CTG	192
Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu	
25 30 35	
GGC CGG CTG GTC CCT CGG GGG CGA GGG GCT GCG GAG GCA GCG ACC CGG	240
Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg	
40 45 50	
AAA CAG CGT ATC ACT GAG ACC GAG TCG CCT TAT CAG GAG CTC CAG GGT	288
Lys Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly	
55 60 65 70	
CAG AGG TCG GAT GTC TAC AGC GAC CTC AAC ACA CAG AGG CCG TAT TAC	336
Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr	
75 80 85	
AAA TGA	342
Lys	

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Gly Gly Leu Glu Pro Cys Ser Arg Leu Leu Leu Leu Pro Leu Leu
-26 -25 -20 -15

Leu Ala Val Ser Gly Leu Arg Pro Val Gln Ala Gln Ala Gln Ser Asp
-10 -5 1 5

Cys Ser Cys Ser Thr Val Ser Pro Gly Val Leu Ala Gly Ile Val Met
10 15 20

Gly Asp Leu Val Leu Thr Val Leu Ile Ala Leu Ala Val Tyr Phe Leu
25 30 35

Gly Arg Leu Val Pro Arg Gly Arg Gly Ala Ala Glu Ala Ala Thr Arg
40 45 50

Lys Gln Arg Ile Thr Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln Gly
55 60 65 70

Gln Arg Ser Asp Val Tyr Ser Asp Leu Asn Thr Gln Arg Pro Tyr Tyr
75 80 85

Lys

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 628 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTGCCTGGA CGCTGCGCCA CATCCCACCG GCCCTTACAC TGTGGTGTCC AGCAGCATCC 60

GGCTTCATGG GGGGACTTGA ACCCTGCAGC AGGCTCCTGC TCCTGCCTCT CCTGCTGGCT 120

GTAAGTGGTC TCCGTCCTGT CCAGGCCAG GCCCAGAGCG ATTGCAGTTG CTCTACGGTG 180

AGCCCGGGCG TGCTGGCAGG GATCGTGATG GGAGACCTGG TGCTGACAGT GCTCATTGCC 240

CTGGCCGTGT ACTTCCTGGG CCGGCTGGTC CCTCGGGGGC GAGGGGCTGC GGAGGCAGCG 300

ACCCGGAAAC AGCGTATCAC TGAGACCGAG TCGCCTTATC AGGAGCTCCA GGGTCAGAGG 360
 TCGGATGTCT ACAGCGACCT CAACACACAG AGGCCGTATT ACAAATGAGC CCGAATCATG 420
 ACAGTCAGCA ACATGATACC TGGATCCAGC CATTCCTGAA GCCCANCTG CACCTCATTC 480
 CAACTCCTAC CGCGATACAG ACCCAGAGAG TGCCATCCCT GAGAGACCAG ACCGCTCCCC 540
 AATACTCTCC TAAAATAAAC ATGAAGCACA AAAAAAAAAA AAAAAAAAAAC TCNGGGGGGG 600
 GGCCCGGTTA NCCAATTTGG NCCTAAAG 628

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 18 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not relevant
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Glu	Ser	Pro	Tyr	Gln	Glu	Leu	Gln	Gly	Gln	Arg	Ser	Asp	Val	Tyr	Ser
1				5				10						15	
Asp Leu															

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 345 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..342

- (ix) FEATURE:
 - (A) NAME/KEY: mat_peptide
 - (B) LOCATION: 79..342

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATG GGG GCT CTG GAG CCC TCC TGG TGC CTT CTG TTC CTT CCT GTC CTC
 Met Gly Ala Leu Glu Pro Ser Trp Cys Leu Leu Phe Leu Pro Val Leu

-26 -25	-20	-15	
CTG ACT GTG GGA GGA TTA AGT CCC GTA CAG GCC CAG AGT GAC ACT TTC			96
Leu Thr Val Gly Gly Leu Ser Pro Val Gln Ala Gln Ser Asp Thr Phe			
-10	-5	1	5
CCA AGA TGC GAC TGT TCT TCC GTG AGC CCT GGT GTA CTG GCT GGG ATT			144
Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ala Gly Ile			
10	15	20	
GTT CTG GGT GAC TTG GTG TTG ACT CTG CTG ATT GCC CTG GCT GTG TAC			192
Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Val Tyr			
25	30	35	
TCT CTG GGC CGC CTG GTC TCC CGA GGT CAA GGG ACA GCG GAA GGG ACC			240
Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu Gly Thr			
40	45	50	
CGG AAA CAA CAC ATT GCT GAG ACT GAG TCG CCT TAT CAG GAG CTT CAG			288
Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln			
55	60	65	70
GGT CAG AGA CCA GAA GTA TAC AGT GAC CTC AAC ACA CAG AGG CAA TAT			336
Gly Gln Arg Pro Glu Val Tyr Ser Asp Leu Asn Thr Gln Arg Gln Tyr			
75	80	85	
TAC AGA TGA			345
Tyr Arg			

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 114 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gly Ala Leu Glu Pro Ser Trp Cys Leu Leu Phe Leu Pro Val Leu	
-26 -25	-20 -15
Leu Thr Val Gly Gly Leu Ser Pro Val Gln Ala Gln Ser Asp Thr Phe	
-10	-5 1 5
Pro Arg Cys Asp Cys Ser Ser Val Ser Pro Gly Val Leu Ala Gly Ile	
10	15 20
Val Leu Gly Asp Leu Val Leu Thr Leu Leu Ile Ala Leu Ala Val Tyr	
25	30 35
Ser Leu Gly Arg Leu Val Ser Arg Gly Gln Gly Thr Ala Glu Gly Thr	
40	45 50
Arg Lys Gln His Ile Ala Glu Thr Glu Ser Pro Tyr Gln Glu Leu Gln	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Ile His Leu Gly His Ile Leu Phe Leu Leu Leu Leu Pro Val Ala
-18 -15 -10 -5

Ala Ala Gln Thr Thr Pro Gly Glu Arg Ser Ser Leu Pro Ala Phe Tyr
1 5 10

Pro Gly Thr Ser Gly Ser Cys Ser Gly Cys Gly Ser Leu Ser Leu Pro
15 20 25 30

Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Ala Ser Leu Leu Ile
35 40 45

Val Gly Ala Val Phe Leu Cys Ala Arg Pro Arg Arg Ser Pro Ala Gln
50 55 60

Asp Gly Lys Val Tyr Ile Asn Met Pro Gly Arg Gly
65 70

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 403 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
(B) LOCATION: 109..345

(ix) FEATURE:

- ```

(A) NAME/KEY: mat_peptide
(B) LOCATION: 163..345

```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

GTCACCATCG GGGTGACATC CGTCCTAGCT GCCTCTCTTC TCCTCTACTG TTCTGAGGAC

60

TTCCCTGGAC CACAGTTTTG GCCAGATCCC TTCAGGTCCC AGCCCAGC ATG GAC CCC  
Met Asp Pro

117



|                                                                 |     |
|-----------------------------------------------------------------|-----|
| CCA GGC TAC CTC CTG TTC CTG CTT CTG CTC CCA GTG GCT GCA AGT CAG | 165 |
| Pro Gly Tyr Leu Leu Phe Leu Leu Leu Leu Pro Val Ala Ala Ser Gln |     |
| -15 -10 -5 1                                                    |     |
| ACA TCG GCA GGT TCC TGC TCC GGA TGT GGG ACT CTG TCT CTG CCA CTC | 213 |
| Thr Ser Ala Gly Ser Cys Ser Gly Cys Gly Thr Leu Ser Leu Pro Leu |     |
| 5 10 15                                                         |     |
| CTG GCA GGC CTA GTG GCT GCA GAT GCG GTC ATG TCA CTC CTA ATT GTA | 261 |
| Leu Ala Gly Leu Val Ala Ala Asp Ala Val Met Ser Leu Leu Ile Val |     |
| 20 25 30                                                        |     |
| GGG GTG GTG TTT GTA TGT ATG CGC CCA CAC GGC AGG CCT GCC CAA GAA | 309 |
| Gly Val Val Phe Val Cys Met Arg Pro His Gly Arg Pro Ala Gln Glu |     |
| 35 40 45                                                        |     |
| GAT GGT AGA GTC TAC ATC AAC ATG CCT GGC AGA GGC TGACCACGGC      | 355 |
| Asp Gly Arg Val Tyr Ile Asn Met Pro Gly Arg Gly                 |     |
| 50 55 60                                                        |     |
| ACCTTCTGAC CCGCTCATCC TGGATCCTGT GGGTTTGGGG TGCCTGGG            | 403 |

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

|                                                                 |  |
|-----------------------------------------------------------------|--|
| Met Asp Pro Pro Gly Tyr Leu Leu Phe Leu Leu Leu Leu Pro Val Ala |  |
| -18 -15 -10 -5                                                  |  |
| Ala Ser Gln Thr Ser Ala Gly Ser Cys Ser Gly Cys Gly Thr Leu Ser |  |
| 1 5 10                                                          |  |
| Leu Pro Leu Leu Ala Gly Leu Val Ala Ala Asp Ala Val Met Ser Leu |  |
| 15 20 25 30                                                     |  |
| Leu Ile Val Gly Val Val Phe Val Cys Met Arg Pro His Gly Arg Pro |  |
| 35 40 45                                                        |  |
| Ala Gln Glu Asp Gly Arg Val Tyr Ile Asn Met Pro Gly Arg Gly     |  |
| 50 55 60                                                        |  |

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 996 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 157..717

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

|                                                                                                                                                       |     |
|-------------------------------------------------------------------------------------------------------------------------------------------------------|-----|
| GGCTTAGCGT GGTCGCGGCC GAGGTGGCAA AAGGAGCATA TTCTCAGGAG ACGGGGCCCC                                                                                     | 60  |
| TGCCTGCCAC ACCAAGCATT AGGCCACCAG GAAGACCCCC ATCTGCAAGC AAGCCTAGCC                                                                                     | 120 |
| TTCCAGGGAG AAAGAGGCCT CTGCAGCTCC TTCATC ATG AAC TGG CAC ATG ATC<br>Met Asn Trp His Met Ile<br>1 5                                                     | 174 |
| ATC TCT GGG CTT ATT GTG GTA GTG CTT AAA GTT GTT GGA ATG ACC TTA<br>Ile Ser Gly Leu Ile Val Val Val Leu Lys Val Val Gly Met Thr Leu<br>10 15 20        | 222 |
| TTT CTA CTT TAT TTC CCA CAG ATT TTT AAC AAA AGT AAC GAT GGT TTC<br>Phe Leu Leu Tyr Phe Pro Gln Ile Phe Asn Lys Ser Asn Asp Gly Phe<br>25 30 35        | 270 |
| ACC ACC ACC AGG AGC TAT GGA ACA GTC TCA CAG ATT TTT GGG AGC AGT<br>Thr Thr Thr Arg Ser Tyr Gly Thr Val Ser Gln Ile Phe Gly Ser Ser<br>40 45 50        | 318 |
| TCC CCA AGT CCC AAC GGC TTC ATT ACC ACA AGG AGC TAT GGA ACA GTC<br>Ser Pro Ser Pro Asn Gly Phe Ile Thr Thr Arg Ser Tyr Gly Thr Val<br>55 60 65 70     | 366 |
| TGC CCC AAA GAC TGG GAA TTT TAT CAA GCA AGA TGT TTT TTC TTA TCC<br>Cys Pro Lys Asp Trp Glu Phe Tyr Gln Ala Arg Cys Phe Phe Leu Ser<br>75 80 85        | 414 |
| ACT TCT GAA TCA TCT TGG AAT GAA AGC AGG GAC TTT TGC AAA GGA AAA<br>Thr Ser Glu Ser Ser Trp Asn Glu Ser Arg Asp Phe Cys Lys Gly Lys<br>90 95 100       | 462 |
| GGA TCC ACA TTG GCA ATT GTC AAC ACG CCA GAG AAA CTG TTT CTT CAG<br>Gly Ser Thr Leu Ala Ile Val Asn Thr Pro Glu Lys Leu Phe Leu Gln<br>105 110 115     | 510 |
| GAC ATA ACT GAT GCT GAG AAG TAT TTT ATT GGC TTA ATT TAC CAT CGT<br>Asp Ile Thr Asp Ala Glu Lys Tyr Phe Ile Gly Leu Ile Tyr His Arg<br>120 125 130     | 558 |
| GAA GAG AAA AGG TGG CGT TGG ATC AAC AAC TCT GTG TTC AAT GGC AAT<br>Glu Glu Lys Arg Trp Arg Trp Ile Asn Asn Ser Val Phe Asn Gly Asn<br>135 140 145 150 | 606 |
| GTT ACC AAT CAG AAT CAG AAT TTC AAC TGT GCG ACC ATT GGC CTA ACA<br>Val Thr Asn Gln Asn Gln Asn Phe Asn Cys Ala Thr Ile Gly Leu Thr<br>155 160 165     | 654 |

AAG ACC TTT GAT GCT GCA TCA TGT GAC ATC AGC TAC CGC AGG ATC TGT 702  
Lys Thr Phe Asp Ala Ala Ser Cys Asp Ile Ser Tyr Arg Arg Ile Cys  
170 175 180

GAG AAG AAT GCC AAA TGATCACAGT TCCCTGTGAC AAGAACTATA CTTGCAACTC 757  
Glu Lys Asn Ala Lys  
185

TTTTTGAATC CATAACAGGT CGTACTGGCC AATGATTACT TTTACTTACC TATCTGTACT 817

ACCAGTAGCG GTCCTTGCCC ATTTGGGAAA CTGAGCTTCT TTCTTCTGCA CTGGGGGACT 877

GGATGCTAGC CATCTCCAGG AGACAGGATC AGTTTTACGG AAACAACCTCA GTTAGTATAG 937

AGATGAGGTC CGCTTCTGTA GTACCTTCCT TCAAATAAAG AAATTTGGTA CCTGCCCCGG 996

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 187 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met Asn Trp His Met Ile Ile Ser Gly Leu Ile Val Val Val Leu Lys  
1 5 10 15

Val Val Gly Met Thr Leu Phe Leu Leu Tyr Phe Pro Gln Ile Phe Asn  
20 25 30

Lys Ser Asn Asp Gly Phe Thr Thr Thr Arg Ser Tyr Gly Thr Val Ser  
35 40 45

Gln Ile Phe Gly Ser Ser Ser Pro Ser Pro Asn Gly Phe Ile Thr Thr  
50 55 60

Arg Ser Tyr Gly Thr Val Cys Pro Lys Asp Trp Glu Phe Tyr Gln Ala  
65 70 75 80

Arg Cys Phe Phe Leu Ser Thr Ser Glu Ser Ser Trp Asn Glu Ser Arg  
85 90 95

Asp Phe Cys Lys Gly Lys Gly Ser Thr Leu Ala Ile Val Asn Thr Pro  
100 105 110

Glu Lys Leu Phe Leu Gln Asp Ile Thr Asp Ala Glu Lys Tyr Phe Ile  
115 120 125

Gly Leu Ile Tyr His Arg Glu Glu Lys Arg Trp Arg Trp Ile Asn Asn  
130 135 140

Ser Val Phe Asn Gly Asn Val Thr Asn Gln Asn Gln Asn Phe Asn Cys  
145 150 155 160

Ala Thr Ile Gly Leu Thr Lys Thr Phe Asp Ala Ala Ser Cys Asp Ile  
165 170 175

Ser Tyr Arg Arg Ile Cys Glu Lys Asn Ala Lys  
180 185

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 896 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 140..709

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 221
- (D) OTHER INFORMATION: /note= "short form variant lacks nucleotides 221-295"

(ix) FEATURE:

- (A) NAME/KEY: misc\_feature
- (B) LOCATION: 29
- (D) OTHER INFORMATION: /note= "short form variant difference at nucleotides 29-35 reads CAGAAGA; 107-109 reads AGA; 128-129 reads AT; 820-826 reads CATAGGT; lacks 859; and 879-880 reads CA"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| AGGACATTAC CGAGCAGGAG CATACATTTC CAGAGCAAGG AGCCCTGCTC GCTGCACCGA | 60  |
| ATATCTTATC AAAAAGACTC CTATCTGTAT GCCAACCCAG ACTTCCCAGA AGAGATCAGA | 120 |
| TCCCTGATCC CCCATCATC ATG AAC TGG CAC ATG ATC ATC TCG GGG CTT ATC  | 172 |
| Met Asn Trp His Met Ile Ile Ser Gly Leu Ile                       |     |
| 1 5 10                                                            |     |
| GTA GTA GTG ATC AAA GTT GTT GGA ATG ACC TTT TTT CTG CTG TAT TTC   | 220 |
| Val Val Val Ile Lys Val Val Gly Met Thr Phe Phe Leu Leu Tyr Phe   |     |
| 15 20 25                                                          |     |
| CCA CAG GTT TTT GGC AAA AGT AAT GAT GGC TTC GTC CCC ACG GAG AGC   | 268 |
| Pro Gln Val Phe Gly Lys Ser Asn Asp Gly Phe Val Pro Thr Glu Ser   |     |
| 30 35 40                                                          |     |
| TAC GGA ACC ACT AGT GTG CAG AAT GTC TCA CAG ATC TTT GGG AGA AAT   | 316 |
| Tyr Gly Thr Thr Ser Val Gln Asn Val Ser Gln Ile Phe Gly Arg Asn   |     |
| 45 50 55                                                          |     |

|                                                                   |     |
|-------------------------------------------------------------------|-----|
| GAC GAA AGT ACC ATG CCT ACA AGG AGC TAT GGA ACA GTC TGT CCC AGA   | 364 |
| Asp Glu Ser Thr Met Pro Thr Arg Ser Tyr Gly Thr Val Cys Pro Arg   |     |
| 60 65 70 75                                                       |     |
| AAC TGG GAT TTT CAC CAA GGA AAA TGC TTT TTC TTC TCC TTC TCC GAA   | 412 |
| Asn Trp Asp Phe His Gln Gly Lys Cys Phe Phe Phe Ser Phe Ser Glu   |     |
| 80 85 90                                                          |     |
| TCA CCT TGG AAA GAC AGC ATG GAT TAT TGT GCA ACA CAA GGA TCC ACA   | 460 |
| Ser Pro Trp Lys Asp Ser Met Asp Tyr Cys Ala Thr Gln Gly Ser Thr   |     |
| 95 100 105                                                        |     |
| CTG GCA ATT GTC AAC ACT CCA GAG AAA CTG AAG TAT CTT CAG GAC ATA   | 508 |
| Leu Ala Ile Val Asn Thr Pro Glu Lys Leu Lys Tyr Leu Gln Asp Ile   |     |
| 110 115 120                                                       |     |
| GCT GGT ATT GAG AAT TAC TTT ATT GGT TTG GTA CGT CAG CCT GGA GAG   | 556 |
| Ala Gly Ile Glu Asn Tyr Phe Ile Gly Leu Val Arg Gln Pro Gly Glu   |     |
| 125 130 135                                                       |     |
| AAA AAG TGG CGC TGG ATC AAC AAC TCT GTG TTC AAT GGC AAT GTT ACC   | 604 |
| Lys Lys Trp Arg Trp Ile Asn Asn Ser Val Phe Asn Gly Asn Val Thr   |     |
| 140 145 150 155                                                   |     |
| AAT CAG GAC CAG AAC TTC GAC TGT GTC ACT ATA GGT CTG ACG AAG ACA   | 652 |
| Asn Gln Asp Gln Asn Phe Asp Cys Val Thr Ile Gly Leu Thr Lys Thr   |     |
| 160 165 170                                                       |     |
| TAT GAT GCT GCA TCA TGT GAA GTC AGC TAT CGC TGG ATC TGC GAA ATG   | 700 |
| Tyr Asp Ala Ala Ser Cys Glu Val Ser Tyr Arg Trp Ile Cys Glu Met   |     |
| 175 180 185                                                       |     |
| AAT GCC AAA TGATCATAGA TCTCTACAAG AGTGAATTTT TACAGAGCTA           | 749 |
| Asn Ala Lys                                                       |     |
| 190                                                               |     |
| GCAAAGGAGA TTAGTTGTGA CTGAAACCAG CCCAGGAAAA TATAGAGCAT CAAAGACTGT | 809 |
| GCCCATCTTC ATAGGTGGGA GTTCCCTATT GAATCCTCAA AGTCAATTTT GTTACTCCAC | 869 |
| AAACATCTTA CCATAGTAAA ACTCCCT                                     | 896 |

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 190 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

|                                                                 |
|-----------------------------------------------------------------|
| Met Asn Trp His Met Ile Ile Ser Gly Leu Ile Val Val Val Ile Lys |
| 1 5 10 15                                                       |

Val Val Gly Met Thr Phe Phe Leu Leu Tyr Phe Pro Gln Val Phe Gly  
20 25 30

Lys Ser Asn Asp Gly Phe Val Pro Thr Glu Ser Tyr Gly Thr Thr Ser  
35 40 45

Val Gln Asn Val Ser Gln Ile Phe Gly Arg Asn Asp Glu Ser Thr Met  
50 55 60

Pro Thr Arg Ser Tyr Gly Thr Val Cys Pro Arg Asn Trp Asp Phe His  
65 70 75 80

Gln Gly Lys Cys Phe Phe Phe Ser Phe Ser Glu Ser Pro Trp Lys Asp  
85 90 95

Ser Met Asp Tyr Cys Ala Thr Gln Gly Ser Thr Leu Ala Ile Val Asn  
100 105 110

Thr Pro Glu Lys Leu Lys Tyr Leu Gln Asp Ile Ala Gly Ile Glu Asn  
115 120 125

Tyr Phe Ile Gly Leu Val Arg Gln Pro Gly Glu Lys Lys Trp Arg Trp  
130 135 140

Ile Asn Asn Ser Val Phe Asn Gly Asn Val Thr Asn Gln Asp Gln Asn  
145 150 155 160

Phe Asp Cys Val Thr Ile Gly Leu Thr Lys Thr Tyr Asp Ala Ala Ser  
165 170 175

Cys Glu Val Ser Tyr Arg Trp Ile Cys Glu Met Asn Ala Lys  
180 185 190